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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent Application

Applicant(s)	Rigoutsos et al.
Docket No.:	YOR920000435US1
Serial No.:	09/712,638
Filing Date:	November 14, 2000
Group:	1631
Examiner:	Cheyne D. Ly

I hereby certify that this paper is being deposited on this date with the U.S. Postal Service as first class mail addressed to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

Signature: Kim Mauro Date: May 22, 2003

#7

Title: Unsupervised Building and Exploitation of Composite Descriptors

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INFORMATION DISCLOSURE STATEMENT

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Pursuant to 37 C.F.R. §§1.56, 1.97 and 1.98, Applicants' attorney wishes to bring to the attention of the Patent and Trademark Office the following document listed on the accompanying PTO Form 1449. A copy of the listed item is enclosed.

1. Altschul et al., "Basic Local Alignment Search Tool," Academic Pres Limited, J. Mol. Biol. 215, pgs 403-410 (1990).
2. Altschul et al., "Issues in Searching Molecular Sequence Databases," Nature Genetics, 6:119-129 (February 1994).
3. Califano et al., "FLASH: A Fast Look-Up Algorithm for String Homology," Proceedings 1993 IEEE Computer Society Conference on Computer Vision and Pattern Recognition, New York, pgs. 353-359 (June 15-18, 1993).
4. Coulson et al., "Protein and Nucleic Acid Sequence Database Searching: A Suitable Case for Parallel Processing," The Computer Journal, vol. 30, no. 5, pgs. 420-424 (1987).
5. Lipman et al., "Rapid and Sensitive Protein Similarity Searches," Science, vol. 227, no. 4693, pgs 1435-1441 (March 22, 1985).
6. Neuwald et al., "Detecting Patterns in Protein Sequences," Academic Press Limited, J. Mol. Biol. 239, pgs. 698-712 (1994).
7. Pearson et al., "Improved Tools for Biological Sequence Comparison," Proc. Nat'l Acad. Sci. USA, vol. 85, pgs. 2444-2448 (April 1988).
8. Rigoutsos et al., "Combinatorial Pattern Discovery in Biological Sequences: The TEIRESEAS Algorithm," Oxford University Press, Bioinformatics, vol. 14, no. 1, pgs. 55-67 (1998).

9. Rigoutsos et al., "Motif Discovery Without Alignment or Enumeration," RECOMB, New York, pgs. 221-227 (1998).
10. Suyama et al., "Searching for Common Sequence Patterns Among Distantly Related Proteins, Protein Engineering, vol. 8, no. 11, pgs. 1075-1080 (1995).
11. Yamaguchi et al., "Protein Motif Discovery from Amino Acid Sequences by Sets of Regular Patterns," Academic Publications, Information Research Report, 95(76):95-FI-38 (July 1995).
12. "Part II, Sequence Analysis," Chapter 9, Pattern Discovery, pgs. 130-169 (September 1993).

Please charge the amount of $180.00 in accordance with 37 C.F.R. §1.17(p) to **IBM Corporation's Deposit Account No. 50-0510**. In the event of non-payment or improper payment of a required fee, the Commissioner is authorized to charge or to credit **IBM Corporation's Deposit Account No. 50-0510** as required to correct the error. Duplicate copies of this letter are enclosed.

The filing of this Information Disclosure Statement shall not be construed as a representation that a search has been made, or as an admission that the information cited is considered to be material to patentability or as a representation that no other material information exists.

Respectfully submitted,

Dated: May 22, 2003

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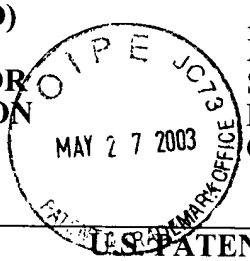
FORM PTO-1449 (MODIFIED)

LIST OF PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT



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U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NO.	DATE	NAME	CLASS/SUBCLASS	FILING DATE IF APPROPRIATE

FOREIGN PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NO.	DATE	COUNTRY	CLASS/SUBCLASS	TRANSLATION YES	TRANSLATION NO

OTHER DOCUMENTS

EXAMINER INITIAL	REF NO.	AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.
		Altschul et al., "Basic Local Alignment Search Tool," Academic Pres Limited, J. Mol. Biol. 215, pgs 403-410 (1990).
		Altschul et al., "Issues in Searching Molecular Sequence Databases," Nature Genetics, 6:119-129 (February 1994).
		Califano et al., "FLASH: A Fast Look-Up Algorithm for String Homology," Proceedings 1993 IEEE Computer Society Conference on Computer Vision and Pattern Recognition, New York, pgs. 353-359 (June 15-18, 1993).
		Coulson et al., "Protein and Nucleic Acid Sequence Database Searching: A Suitable Case for Parallel Processing," The Computer Journal, vol. 30, no. 5, pgs. 420-424 (1987).
		Lipman et al., "Rapid and Sensitive Protein Similarity Searches," Science, vol. 227, no. 4693, pgs 1435-1441 (March 22, 1985).
		Neuwald et al., "Detecting Patterns in Protein Sequences," Academic Press Limited, J. Mol. Biol. 239, pgs. 698-712 (1994).
		Pearson et al., "Improved Tools for Biological Sequence Comparison," Proc. Nat'l Acad. Sci. USA, vol. 85, pgs. 2444-2448 (April 1988).
		Rigoutsos et al., "Combinatorial Pattern Discovery in Biological Sequences: The TEIRESEAS Algorithm," Oxford University Press, Bioinformatics, vol. 14, no. 1, pgs. 55-67 (1998).
		Rigoutsos et al., "Motif Discovery Without Alignment or Enumeration," RECOMB, New York, pgs. 221-227 (1998).
		Suyama et al., "Searching for Common Sequence Patterns Among Distantly Related Proteins, Protein Engineering, vol. 8, no. 11, pgs. 1075-1080 (1995).
		Yamaguchi et al., "Protein Motif Discovery from Amino Acid Sequences by Sets of Regular Patterns," Academic Publications, Information Research Report, 95(76):95-FI-38 (July 1995).
		"Part II, Sequence Analysis," Chapter 9, Pattern Discovery, pgs. 130-169 (September 1993).

Examiner

Date Considered

Examiner: Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and not considered. Include copy of this form with next communication to Applicant.